

SEQUENCE LISTING

<110> Hallahan, David L.

<120> cis-Prenyltransferases from Plants

<130> BC1019 US NA

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<151> 1999-09-21

<160> 37

<170> Microsoft Office 97

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<211> 1388

<212> DNA

<213> Dimorphotheca

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ttaaataggc aatacgtat gccacctaatt atgtcttagtt atgagattct aaagacgtaa 1320  
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<211> 287

<212> PRT

<213> Dimorphotheca

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Ser Asp Thr Thr Gly Gly Ile Asn Ser Leu Glu Glu Arg Ile Thr  
35 40 45

Pro Ala Gly Leu Lys His Glu Leu Met Pro Lys His Val Ala Val Ile  
 50 55 60  
 Met Asp Gly Asn Arg Arg Trp Ala Arg Ser Arg Gly Leu Met Pro Asp  
 65 70 75 80  
 Ala Gly Tyr Met Glu Gly Ala Arg Ser Leu Lys Val Met Val Glu Leu  
 85 90 95  
 Cys Arg Lys Trp Gly Ile Gln Val Leu Thr Val Phe Ala Phe Ser Ala  
 100 105 110  
 Asp Asn Trp Leu Arg Pro Lys Val Glu Val Asp Phe Leu Met Gly Leu  
 115 120 125  
 Ile Glu Ser Val Leu Lys Asp Glu Val Val His Met Ile Lys Glu Gly  
 130 135 140  
 Ile Gln Leu Ser Val Ile Gly Asp Thr Ser Lys Leu Pro Lys Ser Val  
 145 150 155 160  
 Lys Arg Ile Ile Thr Tyr Ala Glu Asn Ile Thr Lys Asn Asn Ser Gln  
 165 170 175  
 Leu Asn Leu Val Val Ala Ile Asn Tyr Ser Gly Lys Tyr Asp Ile Val  
 180 185 190  
 Gln Ala Cys Gln Ser Ile Ala Leu Lys Val Lys Asp Gly Val Ile Gln  
 195 200 205  
 Pro Glu Glu Ile Asn Glu Phe Thr Ile Glu Asn Glu Leu Gly Thr Asn  
 210 215 220  
 Cys Ile Pro Phe Pro His Pro Asp Leu Leu Ile Arg Thr Ser Gly Glu  
 225 230 235 240  
 Leu Arg Val Ser Asn Phe Phe Leu Trp Gln Leu Ala Tyr Thr Glu Leu  
 245 250 255  
 Tyr Phe Ser Glu Thr Leu Trp Pro Asp Phe Gly Glu Asp Glu Leu Leu  
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 His Ala Leu Asn Thr Phe Gln His Arg Arg Arg Arg Tyr Gly Gly  
 275 280 285

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 <211> 1082  
 <212> DNA  
 <213> Calendula officinalis

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 gaagtagaat taccagggggg tctcgaagaa gaactaatgc caaaacacgt tgcattcata 240  
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 tgtcgagtaa gcataatggg gaaaaagacc aacccttccga aatcactaca aaagttatgc 540  
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taataacttgc	ttgtggtaa	gacgagtgtg	gtagaatatac	aataaatgac	tcgtttcggc	960
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<210> 4

<211> 228

<212> PRT

<213> Calendula officinalis

<400> 4

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Val	Glu	Lys	Gly	Trp	Ser	Pro	Met	Thr	Gly	His	Ser	Ala	Met	Arg	Lys
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Thr	Leu	Gln	Ser	Leu	Leu	Phe	Arg	Cys	Ser	Lys	Phe	Lys	Ile	Lys	Ala
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Val	Ser	Ile	Tyr	Ala	Phe	Ser	Thr	Glu	Asn	Trp	Thr	Arg	Pro	Lys	Glu
	50				55					60					

Glu	Val	Asp	Phe	Leu	Met	Glu	Met	Tyr	Glu	Asp	Leu	Leu	Arg	Thr	Asp
	65				70			75					80		

Ala	Glu	Glu	Leu	Leu	Ser	Leu	Gly	Cys	Arg	Val	Ser	Ile	Met	Gly	Lys
	85						90						95		

Lys	Thr	Asn	Leu	Pro	Lys	Ser	Leu	Gln	Lys	Leu	Cys	Ile	Glu	Ile	Glu
		100					105					110			

Glu	Lys	Ser	Arg	Ala	Asn	Ser	Gly	Thr	His	Val	Asn	Tyr	Ala	Leu	Asn
	115						120					125			

Tyr	Ser	Gly	Lys	Tyr	Asp	Ile	Ile	Glu	Ala	Cys	Lys	Ser	Val	Ala	Thr
	130				135					140					

Lys	Val	Lys	Asp	Gly	Val	Ile	Ile	Pro	Lys	Gln	Ile	Asp	Glu	Lys	Tyr
	145				150				155				160		

Phe	Lys	Gln	Glu	Leu	Gly	Thr	Lys	Met	Ile	Asp	Phe	Pro	Tyr	Pro	Asp
	165						170					175			

Leu	Val	Ile	Arg	Thr	Ser	Gly	Glu	Ile	Arg	Leu	Ser	Asn	Phe	Met	Leu
	180						185					190			

Trp	Gln	Met	Ala	Tyr	Ser	Glu	Leu	Tyr	Phe	Thr	Asp	Lys	Tyr	Phe	Pro
	195						200					205			

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Val Arg Lys Cys  
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<211> 1071

<212> DNA

<213> Hevea brasiliensis

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taagtca	attaaggaa	aatgaaatta	tacaacgg	agaggccaag	tgtgttcaga	180
cttttagg	agtatatgag	aaaagggtt	tatagcatcc	taacccaggg	tcccatccct	240
actcatatt	ccttcata	ggatggaaac	aggaggtt	ctaagaagca	taaactgc	300
gaaggaggt	gtcataaggc	tggatttt	gctcttctg	acgtactaac	ttattgctat	360
gagttagg	tgaatatgc	gactatctat	gccttagca	tcgataattt	tcgaaggaaa	420
cctcatgagg	ttcagtagt	aatggatcta	atgctggaga	agattgaagg	gatgatcatg	480
gaagaaagta	tcatcaatgc	atatgatatt	tgctacgtt	ttgtgggtaa	cctgaagctt	540
ttaagtgagc	ccgtcaagac	cgcagcagat	aagattatga	gggctactgc	caacaattcc	600
aatatgtgtc	ttctcattgc	tgtatgctat	acttcaactg	atgagatcgt	gcatgtcttt	660
gaagaatcct	ctgaatgaa	ctccaaatgaa	gtttagtaca	atcaagaattt	gggaggaggca	720
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tattctcc	atgcactgt	gccagagatt	ggtcttcgac	acgtgggtgt	gtcagtaatt	960
aacttccaac	gtcattattc	ttacttggag	aaacataagg	aatacttaaa	ataatttggt	1020
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<211> 290

<212> PRT

<213> *Hevea brasiliensis*

<400> 6

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20 25 30

Pro Thr His Ile Ala Phe Ile Leu Asp Gly Asn Arg Arg Phe Ala Lys  
35 40 45

Lys His Lys Leu Pro Glu Gly Gly Gly His Lys Ala Gly Phe Leu Ala  
50 55 60

Leu Leu Asn Val Leu Thr Tyr Cys Tyr Glu Leu Gly Val Lys Tyr Ala  
65 70 75 80

Thr Ile Tyr Ala Phe Ser Ile Asp Asn Phe Arg Arg Lys Pro His Glu  
85 90 95

Val Gln Tyr Val Met Asp Leu Met Leu Glu Lys Ile Glu Gly Met Ile  
100 105 110

Met Glu Glu Ser Ile Ile Asn Ala Tyr Asp Ile Cys Val Arg Phe Val  
115 120 125

Gly Asn Leu Lys Leu Leu Ser Glu Pro Val Lys Thr Ala Ala Asp Lys  
 130 135 140

Ile Met Arg Ala Thr Ala Asn Asn Ser Lys Cys Val Leu Leu Ile Ala  
145 150 155 160

Val Cys Tyr Thr Ser Thr Asp Glu Ile Val His Ala Val Glu Glu Ser  
165 170 175

Ser Glu Leu Asn Ser Asn Glu Val Cys Asn Asn Gln Glu Leu Glu Glu  
180 185 190

Ala Asn Ala Thr Gly Ser Ser Thr Val Ile Gln Thr Glu Asn Met Glu  
195 200 205

Ser Tyr Ser Gly Ile Lys Leu Val Asp Leu Glu Lys Asn Thr Tyr Ile  
210 215 220

Asn Pro Tyr Pro Asp Val Leu Ile Arg Thr Ser Gly Glu Thr Arg Leu  
225 230 235 240

Ser Asn Tyr Leu Leu Trp Gln Thr Thr Asn Cys Ile Leu Tyr Ser Pro  
245 250 255

Tyr Ala Leu Trp Pro Glu Ile Gly Leu Arg His Val Val Trp Ser Val  
260 265 270

Ile Asn Phe Gln Arg His Tyr Ser Tyr Leu Glu Lys His Lys Glu Tyr  
275 280 285

Leu Lys  
290

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<211> 1000

<212> DNA

<213> Hevea brasiliensis

<400> 7

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tcc	ttactca	tattgc	tttc	aaac	180
tgcc	cagaagg	agg	ggat	ctt	240
gctat	gagtt	agg	gtt	atc	300
ggaa	accta	agg	ttt	act	360
tcat	gga	atc	atc	atc	420
agct	tttaa	atc	atc	atc	480
attcc	aatg	atc	atc	atc	540
ctgtt	gtt	atc	atc	atc	600
aggc	aaatgc	atc	atc	atc	660
gaata	aaact	atc	atc	atc	720
ttcga	acttc	atc	atc	atc	780
tact	gtt	atc	atc	atc	840
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<210> 8

<211> 290

<212> PRT

<213> Hevea brasiliensis

<400> 8

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Lys Tyr Met Arg Lys Gly Leu Tyr Ser Ile Leu Thr Gln Gly Pro Ile  
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Pro Thr His Ile Ala Phe Ile Leu Asp Gly Asn Arg Arg Phe Ala Lys  
35 40 45

Lys His Lys Leu Pro Glu Gly Gly His Lys Ala Gly Phe Leu Ala  
50 55 60

Leu Leu Asn Val Leu Thr Tyr Cys Tyr Glu Leu Gly Val Lys Tyr Ala  
 65 70 75 80  
 Thr Ile Tyr Ala Phe Ser Ile Asp Asn Phe Arg Arg Lys Pro His Glu  
 85 90 95  
 Val Gln Tyr Val Met Asp Leu Met Leu Glu Lys Ile Glu Gly Met Ile  
 100 105 110  
 Met Glu Glu Ser Ile Ile Asn Ala Tyr Asp Ile Cys Val Arg Phe Val  
 115 120 125  
 Gly Asn Leu Lys Leu Leu Ser Glu Pro Val Lys Thr Ala Ala Asp Lys  
 130 135 140  
 Ile Met Arg Ala Thr Ala Asn Asn Ser Lys Cys Val Leu Leu Ile Ala  
 145 150 155 160  
 Val Cys Tyr Thr Ser Thr Asp Glu Ile Val His Ala Val Glu Glu Ser  
 165 170 175  
 Ser Glu Leu Asn Ser Asn Glu Val Cys Asn Asn Gln Glu Leu Glu Glu  
 180 185 190  
 Ala Asn Ala Thr Gly Ser Ser Thr Val Ile Gln Thr Glu Asn Met Glu  
 195 200 205  
 Ser Tyr Ser Gly Ile Lys Leu Val Asp Leu Glu Lys Asn Thr Tyr Ile  
 210 215 220  
 Asn Pro Tyr Pro Asp Val Leu Ile Arg Thr Ser Gly Glu Thr Arg Leu  
 225 230 235 240  
 Ser Asn Tyr Leu Leu Trp Gln Thr Thr Asn Cys Ile Leu Tyr Ser Pro  
 245 250 255  
 Tyr Ala Leu Trp Pro Glu Ile Gly Leu Arg His Val Val Trp Ser Val  
 260 265 270  
 Ile Asn Phe Gln Arg His Tyr Ser Tyr Leu Glu Lys His Lys Glu Tyr  
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 Leu Lys  
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 cataatggat gaaaccggta ggttgctaa gaagcacaaa atgaaagaag cagaaggta 240  
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 aataaatctt gcagacccctt agaaaaacac ctacgttaat cctcatcctt atgtcttgat 780

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 Pro Thr His Leu Ala Phe Ile Met Asp Gly Asn Arg Arg Phe Ala Lys  
 35 40 45  
 Lys His Lys Met Lys Glu Ala Glu Gly Tyr Lys Ala Gly Tyr Leu Ala  
 50 55 60  
 Leu Leu Arg Thr Leu Thr Tyr Cys Tyr Glu Leu Gly Val Arg Tyr Val  
 65 70 75 80  
 Thr Ile Tyr Ala Phe Ser Ile Asp Asn Phe Arg Arg Gln Pro Arg Glu  
 85 90 95  
 Val Gln Cys Val Met Asn Leu Met Met Glu Lys Ile Glu Glu Ile Ile  
 100 105 110  
 Val Glu Glu Ser Ile Met Asn Ala Tyr Asp Val Gly Val Arg Ile Val  
 115 120 125  
 Gly Asn Leu Asn Leu Leu Asp Glu Pro Ile Arg Ile Ala Ala Glu Lys  
 130 135 140  
 Ile Met Arg Ala Thr Ala Asn Asn Ser Gly Phe Val Leu Leu Ile Ala  
 145 150 155 160  
 Val Ala Tyr Ser Ser Thr Asp Glu Ile Gly His Ala Val Glu Glu Ser  
 165 170 175  
 Ser Lys Asp Lys Leu Asn Ser Asn Glu Val Cys Asn Asn Gly Ile Glu  
 180 185 190  
 Ala Glu Gln Glu Phe Lys Glu Ala Asn Gly Thr Gly Asn Ser Val Ile  
 195 200 205  
 Pro Val Gln Lys Thr Glu Ser Tyr Ser Gly Ile Asn Leu Ala Asp Leu  
 210 215 220  
 Glu Lys Asn Thr Tyr Val Asn Pro His Pro Asp Val Leu Ile Arg Thr  
 225 230 235 240  
 Ser Gly Leu Ser Arg Leu Ser Asn Tyr Leu Leu Trp Gln Thr Ser Asn  
 245 250 255  
 Cys Ile Leu Tyr Ser Pro Phe Ala Leu Trp Pro Glu Ile Gly Leu Arg  
 260 265 270  
 His Leu Val Trp Thr Val Met Asn Phe Gln Arg His His Ser Tyr Leu  
 275 280 285

Glu Lys His Lys Glu Tyr Leu Lys  
290 295

<210> 11  
<211> 1232  
<212> DNA  
<213> Vitis sp

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ctcggtttc gcattttcct atgataattt gtcgttcc gaaggggagg ttggttttct 480  
tatgagctt atcgaaaagag tggtcaaagc tgagctgcca attttgggag ggaaggcatt 540  
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gttggccaa atagcttaca ctgaaactttt ctttttttagc acactgtggc ctgattttgg 900  
gaaggatgag tttgtggagg ccttaagttc ttttcagaaa aggcaagagac gatatgggg 960  
gcaaaaactga gttactaat tacatataga tcccccaattt ctgctccattt catatggaga 1020  
acttgtatac cattatatga agttaaattt ctgagaattt acttattaca cacagatccc 1080  
caacctatac tccatttata tggaaaactt gtaccattat atgaaactca ttcttcagaa 1140  
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<212> PRT  
<213> Vitis sp

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Phe Lys Ser Lys His Ser Ser Cys Thr Phe Arg Ser Asn Arg Ile Asp  
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Ser Phe Ser Phe Pro Pro Ile Ser Val Pro Arg Phe His Lys Leu Arg  
35 40 45  
  
Thr Ala Lys Thr Asp Val Val Gly Glu Glu Ala Arg Glu Val Asn  
50 55 60  
  
Glu Arg Ala Glu Glu Phe Pro Asp Gly Leu Arg Arg Glu Leu Met Pro  
65 70 75 80  
  
Glu His Val Ala Val Ile Met Asp Gly Asn Val Arg Trp Ala Gln Lys  
85 90 95  
  
Arg Gly Leu Pro Ala Ala Ser Gly His Gln Ala Gly Val Arg Ser Leu  
100 105 110  
  
Arg Glu Leu Val Glu Leu Cys Cys Lys Trp Gly Ile Lys Val Leu Ser  
115 120 125

Val	Phe	Ala	Phe	Ser	Tyr	Asp	Asn	Trp	Ser	Arg	Ser	Glu	Gly	Glu	Val
130						135					140				
Gly	Phe	Leu	Met	Ser	Leu	Ile	Glu	Arg	Val	Val	Lys	Ala	Glu	Leu	Pro
145					150				155					160	
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Ala	Ser	Glu	Gln	Leu	Gln	Leu	Ile	Ile	Asp	Val	Glu	Glu	Thr	Thr	Lys
		180					185					190			
Glu	Asn	Ser	Arg	Leu	Gln	Phe	Ile	Val	Ala	Leu	Ser	Tyr	Ser	Gly	Gln
		195				200					205				
Cys	Asp	Ile	Leu	Gln	Ala	Cys	Lys	Asn	Ile	Gly	His	Lys	Val	Lys	Asp
	210					215				220					
Gly	Leu	Ile	Glu	Pro	Glu	Asp	Ile	Asn	Lys	Ser	Leu	Ile	Glu	Gln	Glu
225			230					235					240		
Leu	Gln	Thr	Asn	Cys	Thr	Glu	Phe	Pro	Phe	Pro	Asp	Leu	Leu	Ile	Arg
		245				250						255			
Thr	Ser	Gly	Glu	Leu	Arg	Val	Ser	Asn	Phe	Met	Leu	Trp	Gln	Ile	Ala
		260					265				270				
Tyr	Thr	Glu	Leu	Cys	Phe	Phe	Ser	Thr	Leu	Trp	Pro	Asp	Phe	Gly	Lys
	275					280					285				
Asp	Glu	Phe	Val	Glu	Ala	Leu	Ser	Ser	Phe	Gln	Lys	Arg	Gln	Arg	Arg
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Tyr	Gly	Gly	Arg	Asn											
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<210>	13														
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<211> 252

<212> PRT

<213> Oryza sativa

<400> 14

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20 25 30

Ala Leu Ile Ala Ser Leu Leu Tyr Cys Tyr Glu Met Gly Val Lys Tyr  
35 40 45

Ile Thr Val Tyr Ala Phe Ser Ile Asp Asn Phe Lys Arg Asp Pro Thr  
50 55 60

Glu Val Lys Ser Leu Met Glu Leu Met Glu Glu Lys Ile Asn Glu Leu  
65 70 75 80

Leu Glu Asn Arg Asn Val Ile Asn Lys Val Asn Cys Lys Ile Asn Phe  
85 90 95

Trp Gly Asn Leu Asp Met Leu Ser Lys Ser Val Arg Val Ala Ala Glu  
100 105 110

Lys Leu Met Ala Thr Thr Ala Glu Asn Thr Gly Leu Val Phe Ser Val  
115 120 125

Cys Met Pro Tyr Asn Ser Thr Ser Glu Ile Val Asn Ala Val Asn Lys  
130 135 140

Val Cys Ala Glu Arg Arg Asp Ile Leu Gln Arg Glu Asp Ala Asp Ser  
145 150 155 160

Val Ala Asn Asn Gly Val Tyr Ser Asp Ile Ser Val Ala Asp Leu Asp  
165 170 175

Arg His Met Tyr Ser Ala Gly Cys Pro Asp Pro Asp Ile Val Ile Arg  
180 185 190

Thr Ser Gly Glu Thr Arg Leu Ser Asn Phe Leu Leu Trp Gln Thr Thr  
195 200 205

Phe Ser His Leu Gln Asn Pro Asp Pro Leu Trp Pro Glu Phe Ser Phe  
210 215 220

Lys His Leu Val Trp Ala Ile Leu Gln Tyr Gln Arg Val His Pro Ser  
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Ile Glu Gln Ser Arg Asn Leu Ala Lys Lys Gln Leu  
245 250

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<211> 900

<212> DNA

<213> Oryza sativa

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gctgtccctc cgtatggccc aatgcctaag catattgcat ttattatgga tggtaaccgt 180

agatatgcta aattcaggag tatccaggaa ggctctggc acaggggtggg cttctctgct 240  
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 atcaacttct gggggactt ggacatgttg agcaaattcag tgagggttagc agctgagaaa 480  
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 aatccagacc ctcttggcc ggagttctt ttcaagcacc ttgtctggc cataactccag 840  
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 <213> Oryza sativa

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 20 25 30

Asn Phe Ile Arg Lys Cys Ile Val Ala Val Leu Ser Tyr Gly Pro Met  
 35 40 45

Pro Lys His Ile Ala Phe Ile Met Asp Gly Asn Arg Arg Tyr Ala Lys  
 50 55 60

Phe Arg Ser Ile Gln Glu Gly Ser Gly His Arg Val Gly Phe Ser Ala  
 65 70 75 80

Leu Ile Ala Ser Leu Leu Tyr Cys Tyr Glu Met Gly Val Lys Tyr Ile  
 85 90 95

Thr Val Tyr Ala Phe Ser Ile Asp Asn Phe Lys Arg Asp Pro Thr Glu  
 100 105 110

Val Lys Ser Leu Met Glu Leu Met Glu Glu Lys Ile Asn Glu Leu Leu  
 115 120 125

Glu Asn Arg Asn Val Ile Asn Lys Val Asn Cys Lys Ile Asn Phe Trp  
 130 135 140

Gly Asn Leu Asp Met Leu Ser Lys Ser Val Arg Val Ala Ala Glu Lys  
 145 150 155 160

Leu Met Ala Thr Thr Ala Glu Asn Thr Gly Leu Val Phe Ser Val Cys  
 165 170 175

Met Pro Tyr Asn Ser Thr Ser Glu Ile Val Asn Ala Val Asn Lys Val  
 180 185 190

Cys Ala Glu Arg Arg Asp Ile Leu Gln Arg Glu Asp Ala Asp Ser Val  
 195 200 205

Ala Asn Asn Gly Val Tyr Ser Asp Ile Ser Val Ala Asp Leu Asp Arg  
 210 215 220

His Met Tyr Ser Ala Gly Cys Pro Asp Pro Asp Ile Val Ile Arg Thr  
 225 230 235 240

Ser Gly Glu Thr Arg Leu Ser Asn Phe Leu Leu Trp Gln Thr Thr Phe  
245 250 255

Ser His Leu Gln Asn Pro Asp Pro Leu Trp Pro Glu Phe Ser Phe Lys  
260 265 270

His Leu Val Trp Ala Ile Leu Gln Tyr Gln Arg Val His Pro Ser Ile  
275 280 285

Glu Gln Ser Arg Asn Leu Ala Lys Lys Gln Leu  
290 295

<210> 17

<211> 1028

<212> DNA

<213> Glycine max

<400> 17

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attctcacta	ttatcactat	cgttatcggt	atcggttgc	tcatccttgc	catcaccgtt	180
cccaaacaca	gagtttatac	gtctcgaaagc	gcgggtccgc	cattgcgaag	tgtcacgtgc	240
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cggcggact	cgcggcggag	atgatgcca	agcatgtggc	ggtgataatg	gacggaaacg	360
ggaggtggc	gaaggtaag	gggctgccac	catggcgccc	gcaccaggcg	ggggtgcaat	420
cgctgaggaa	aatggtgagg	ctgtgttgc	gctggggat	taagttcta	acggttttcg	480
cgttctctac	ggataactgg	gttcgcggca	aggtggaggt	tgatttcttg	atgaggctgt	540
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tgattggaga	ttcatcaagg	ttgcctgagt	ctttaaaaag	aatgatagct	agtgcagaag	660
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atgatgttgt	gcaagcatgt	aaaagtgtag	ccaagaaagt	caaagatgtt	cacattcaact	780
tggatgacat	aaacgaaaac	attattgaac	aagaatttggc	aactaattgt	actgagttc	840
cttattcctga	tctactaata	cgaacttagt	gcgagcttag	agtgagtaac	ttcttgttgt	900
ggcaatttagc	ctacacagaa	ctttatTTA	atcgggaact	ctggccagat	tttgggaagg	960
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<211> 322

<212> PRT

<213> Glycine max

<400> 18

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Pro Ser Cys Tyr Tyr Ser His Tyr Tyr His Tyr Arg Tyr Arg Tyr Arg						
20	25	30				

Cys Tyr His Pro Phe His His Arg Ser Gln Thr Gln Ser Leu Ile Val						
35	40	45				

Ser Lys Arg Gly Ser Ala Ile Ala Lys Cys His Ala Asp Ser Val Thr						
50	55	60				

Leu Arg Asp Asp Gly Val Ser Leu Ala Gln Glu Ser Leu Glu Pro Leu						
65	70	75	80			

Pro Ala Glu Leu Ala Ala Glu Met Met Pro Lys His Val Ala Val Ile						
85	90	95				

Met Asp Gly Asn Gly Arg Trp Ala Lys Val Lys Gly Leu Pro Pro Ser  
 100 105 110  
 Ala Gly His Gln Ala Gly Val Gln Ser Leu Arg Lys Met Val Arg Leu  
 115 120 125  
 Cys Cys Ser Trp Gly Ile Lys Val Leu Thr Val Phe Ala Phe Ser Thr  
 130 135 140  
 Asp Asn Trp Val Arg Pro Lys Val Glu Val Asp Phe Leu Met Arg Leu  
 145 150 155 160  
 Phe Glu Arg Thr Ile Asn Ser Glu Val Gln Thr Phe Lys Arg Glu Gly  
 165 170 175  
 Ile Arg Ile Ser Val Ile Gly Asp Ser Ser Arg Leu Pro Glu Ser Leu  
 180 185 190  
 Lys Arg Met Ile Ala Ser Ala Glu Glu Asp Thr Lys Gln Asn Ser Arg  
 195 200 205  
 Phe Gln Leu Ile Val Ala Val Gly Tyr Ser Gly Lys Tyr Asp Val Val  
 210 215 220  
 Gln Ala Cys Lys Ser Val Ala Lys Lys Val Lys Asp Gly His Ile His  
 225 230 235 240  
 Leu Asp Asp Ile Asn Glu Asn Ile Ile Glu Gln Glu Leu Glu Thr Asn  
 245 250 255  
 Cys Thr Glu Phe Pro Tyr Pro Asp Leu Leu Ile Arg Thr Ser Gly Glu  
 260 265 270  
 Leu Arg Val Ser Asn Phe Leu Leu Trp Gln Leu Ala Tyr Thr Glu Leu  
 275 280 285  
 Tyr Phe Asn Arg Glu Leu Trp Pro Asp Phe Gly Lys Asp Glu Phe Val  
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 His Ser  
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 <213> Triticum aestivum  
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 gggaaactcgc ggtggggcggc agcgcggggc ctggccggca cggacgggca cgagcacggg 180  
 atgcgcgcgc tgatgaggac ggtgcggctc tcccgcgcct ggggcattcg cgtcctcacc 240  
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 ctacgtataa tcggtgaccg ctcaggctg cggatctctg tgcagaagac tgcacgagac 420  
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 aaaaaaa 1026

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 <212> PRT  
 <213> *Triticum aestivum*

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 20 25 30

Arg His Val Ala Leu Val Met Asp Gly Asn Ser Arg Trp Ala Ala Ala  
 35 40 45

Arg Gly Leu Pro Pro Thr Asp Gly His Glu His Gly Met Arg Ala Leu  
 50 55 60

Met Arg Thr Val Arg Leu Ser Arg Ala Trp Gly Ile Arg Val Leu Thr  
 65 70 75 80

Ala Phe Gly Phe Ser Leu Glu Asn Trp Asn Arg Pro Lys Ala Glu Val  
 85 90 95

Asp Phe Leu Met Ala Leu Ile Glu Arg Phe Ile Asn Asp Asn Leu Ala  
 100 105 110

Glu Phe Leu Arg Glu Gly Thr Arg Leu Arg Ile Ile Gly Asp Arg Ser  
 115 120 125

Arg Leu Pro Ile Ser Val Gln Lys Thr Ala Arg Asp Ala Glu Glu Ala  
 130 135 140

Thr Arg Asn Asn Ser Gln Leu Asp Leu Val Leu Ala Ile Ser Tyr Ser  
 145 150 155 160

Gly Arg Met Asp Ile Val Gln Ala Cys Arg Asn Leu Ala Gln Lys Val  
 165 170 175

Asp Ala Lys Leu Leu Arg Pro Glu Asp Ile Asp Glu Ser Leu Phe Ala  
 180 185 190

Asp Glu Leu Gln Thr Ser Glu Thr Ser Cys Pro Asp Leu Leu Ile Arg  
 195 200 205

Thr Ser Gly Glu Leu Arg Leu Ser Asn Phe Leu Leu Trp Gln Ser Ala  
 210 215 220

Tyr Ser Glu Leu Phe Phe Thr Asp Thr Leu Trp Pro Asp Phe Gly Glu  
 225 230 235 240

Ala Gln Tyr Leu Gln Ala Met Met Ala Phe Gln Ser Arg Asp Arg Arg  
 245 250 255

Phe Gly Arg Arg Lys Asn Asn Ala Ala Leu  
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<212> PRT  
<213> Artificial Sequence

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<220>  
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<222> (10)  
<223> X = any amino acid

<300>  
<301> Apfel, C. M.  
<302> Use of Genomics to Identify Bacterial Undecaprenyl Pyrophosphate Synthetase: Cloning, Expression, and Characterization of the Essential uppS Gene  
<303> J. Bacteriol.  
<304> 81  
<306> 483-492  
<307> 1999

<400> 21  
His Xaa Xaa Met Asp Gly Asn Xaa Arg Xaa Ala  
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<210> 22  
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<212> PRT  
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<220>  
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Leu Trp Gln Xaa Xaa Tyr Xaa Glu  
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<210> 23  
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<212> DNA  
<213> Micrococcus luteus

<300>  
<301> Shimizu, N.  
<302> Molecular Cloning, Expression, and Purification of Undecprenyl Diphosphate Synthase: No Sequence Similarity between E- and Z-prenyl Diphosphate Synthases  
<303> J. Biol. Chem.  
<304> 273  
<306> 19476-19481  
<307> 1998

<400> 23  
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ccgcgcataa aaggacatta tgaaggcatg cagaccgtaa agaaaaatcac aagatatgct 180  
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<212> PRT  
<213> Micrococcus luteus

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Arg Trp Ala Lys Gln Lys Lys Met Pro Arg Ile Lys Gly His Tyr Glu  
35 40 45

Gly Met Gln Thr Val Lys Lys Ile Thr Arg Tyr Ala Ser Asp Leu Gly  
50 55 60

Val Lys Tyr Leu Thr Leu Tyr Ala Phe Ser Thr Glu Asn Trp Ser Arg  
65 70 75 80

Pro Lys Asp Glu Val Asn Tyr Leu Met Lys Leu Pro Gly Asp Phe Leu  
                   85                         90                         95  
  
 Asn Thr Phe Leu Pro Glu Leu Ile Glu Lys Asn Val Lys Val Glu Thr  
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 Ile Gly Phe Ile Asp Asp Leu Pro Asp His Thr Lys Lys Ala Val Leu  
                   115                     120                         125  
  
 Glu Ala Lys Glu Lys Thr Lys His Asn Thr Gly Leu Thr Leu Val Phe  
                   130                     135                         140  
  
 Ala Leu Asn Tyr Gly Gly Arg Lys Glu Ile Ile Ser Ala Val Gln Leu  
                   145                     150                         155                 160  
  
 Ile Ala Glu Arg Tyr Lys Ser Gly Glu Ile Ser Leu Asp Glu Ile Ser  
                   165                     170                         175  
  
 Glu Thr His Phe Asn Glu Tyr Leu Phe Thr Ala Asn Met Pro Asp Pro  
                   180                     185                         190  
  
 Glu Leu Leu Ile Arg Thr Ser Gly Glu Glu Arg Leu Ser Asn Phe Leu  
                   195                     200                         205  
  
 Ile Trp Gln Cys Ser Tyr Ser Glu Phe Val Phe Ile Asp Glu Phe Trp  
                   210                     215                         220  
  
 Pro Asp Phe Asn Glu Glu Ser Leu Ala Gln Cys Ile Ser Ile Tyr Gln  
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 caggcatcga gtaaggGCgt acgcatcgaa ttgctggatt gtttatGGCC agagTTTGG 720  
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 <212> PRT  
 <213> *Saccharomyces cerevisiae*

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 Arg His Val Gly Phe Ile Met Asp Gly Asn Arg Arg Phe Ala Arg Lys  
 35 40 45  
 Lys Glu Met Asp Val Lys Glu Gly His Glu Ala Gly Phe Val Ser Met  
 50 55 60  
 Ser Arg Ile Leu Glu Leu Cys Tyr Glu Ala Gly Val Asp Thr Ala Thr  
 65 70 75 80  
 Val Phe Ala Phe Ser Ile Glu Asn Phe Lys Arg Ser Ser Arg Glu Val  
 85 90 95  
 Glu Ser Leu Met Thr Leu Ala Arg Glu Arg Ile Arg Gln Ile Thr Glu  
 100 105 110  
 Arg Gly Glu Leu Ala Cys Lys Tyr Gly Val Arg Ile Lys Ile Ile Gly  
 115 120 125  
 Asp Leu Ser Leu Leu Asp Lys Ser Leu Leu Glu Asp Val Arg Val Ala  
 130 135 140  
 Val Glu Thr Thr Lys Asn Asn Lys Arg Ala Thr Leu Asn Ile Cys Phe  
 145 150 155 160  
 Pro Tyr Thr Gly Arg Glu Glu Ile Leu His Ala Met Lys Glu Thr Ile  
 165 170 175  
 Val Gln His Lys Lys Gly Ala Ala Ile Asp Glu Ser Thr Leu Glu Ser  
 180 185 190  
 His Leu Tyr Thr Ala Gly Val Pro Pro Leu Asp Leu Leu Ile Arg Thr  
 195 200 205  
 Ser Gly Val Ser Arg Leu Ser Asp Phe Leu Ile Trp Gln Ala Ser Ser  
 210 215 220  
 Lys Gly Val Arg Ile Glu Leu Leu Asp Cys Leu Trp Pro Glu Phe Gly  
 225 230 235 240  
 Pro Ile Arg Met Ala Trp Ile Leu Leu Lys Phe Ser Phe His Lys Ser  
 245 250 255  
 Phe Leu Asn Lys Glu Tyr Arg Leu Glu Glu Gly Asp Tyr Asp Glu Glu  
 260 265 270  
 Thr Asn Gly Asp Pro Ile Asp Leu Lys Glu Lys Lys Leu Asn  
 275 280 285  
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 <212> DNA  
 <213> *Saccharomyces cerevisiae*  
 <300>  
 <308> AB013498

<400> 27

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atgtcattaa	gcttgtttc	atggtttat	gtaaatcttc	agaatatttt	gataaaagca	180
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Phe	Gln	Arg	Val	Phe	Ala	Trp	Val	Met	Ser	Leu	Ser	Leu	Phe	Ser	Trp
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Phe	Tyr	Val	Asn	Leu	Gln	Asn	Ile	Leu	Ile	Lys	Ala	Leu	Arg	Val	Gly
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Pro	Val	Pro	Glu	His	Val	Ser	Phe	Ile	Met	Asp	Gly	Asn	Arg	Arg	Tyr
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Ala	Lys	Ser	Arg	Arg	Leu	Pro	Val	Lys	Lys	Gly	His	Glu	Ala	Gly	Gly
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Leu	Thr	Leu	Leu	Thr	Leu	Leu	Tyr	Ile	Cys	Lys	Arg	Leu	Gly	Val	Lys
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Cys	Val	Ser	Ala	Tyr	Ala	Phe	Ser	Ile	Glu	Asn	Phe	Asn	Arg	Pro	Lys
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Glu	Glu	Val	Asp	Thr	Leu	Met	Asn	Leu	Phe	Thr	Val	Lys	Leu	Asp	Glu
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Phe	Ala	Lys	Arg	Ala	Lys	Asp	Tyr	Lys	Asp	Pro	Leu	Tyr	Gly	Ser	Lys
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Ile	Arg	Ile	Val	Gly	Asp	Gln	Ser	Leu	Leu	Ser	Pro	Glu	Met	Arg	Lys
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Lys	Ile	Lys	Lys	Val	Glu	Glu	Ile	Thr	Gln	Asp	Gly	Asp	Asp	Phe	Thr
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Leu	Phe	Ile	Cys	Phe	Pro	Tyr	Thr	Ser	Arg	Asn	Asp	Met	Leu	His	Thr
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Asn Ile Arg Lys Phe Thr Asn Lys Met Tyr Met Gly Phe His Ser Asn  
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Lys Cys Glu Leu Leu Ile Arg Thr Ser Gly His Arg Arg Leu Ser Asp  
245 250 255

Tyr Met Leu Trp Gln Val His Glu Asn Ala Thr Ile Glu Phe Ser Asp  
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Thr Leu Trp Pro Asn Phe Ser Phe Ala Met Tyr Leu Met Ile Leu  
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Lys Trp Ser Phe Phe Ser Thr Ile Gln Lys Tyr Asn Glu Lys Asn His  
290 295 300

Ser Leu Phe Glu Lys Ile His Glu Ser Val Pro Ser Ile Phe Lys Lys  
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